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Genetic diversity among papaya accessions

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Genetic diversity studies provide fundamental information for characterization, conservation and utilization of available genetic resources in plant genetic improvement programs. To evaluate the genetic divergence among papaya accessions, 17 morphoagronomic variables from 59 accessions of the active germplasm bank were evaluated in an experiment at Santa Teresinha Farm, belonging to Caliman Agrícola S/A, in Linhares-ES, Brazil. The experiment was conducted in a randomized block design with two replicates. The divergence between the accessions was estimated using the Tocher optimization method and the agglomerative hierarchical approach based on the Unweighted Pair-Group Method Using an Arithmetic Average. (UPGMA). There was significant difference for all the variables evaluated, showing variability among the accessions. The variables plant height, first fruit insertion height, greatest thickness of fruit pulp, fruit diameter, and fruit length had heritability above 80%, indicating expressive gains in the simple process of selection. Genetic variability was found among the accessions, and Americano, short-peduncle-STZ-03 and Califlora 209 were the most divergent. The optimization methods Tocher and hierarchical based on UPGMA were partially concordant for the formation of heterotic groups of papaya accessions. The variables fruit mass, fruit diameter and plant height contributed the most to the genetic diversity.

Keywords: *Carica papaya* L., genetic variability, multivariate analysis.

INTRODUCTION

Papaya (*Carica papaya* L.) is one of the most cultivated fruits in tropical and subtropical regions of the world.

Papaya fruits are widely used in food diets because they are excellent sources of calcium, pro-vitamin A and

vitamin C (Serrano and Cattaneo, 2010). Brazil is one of the world's largest producers of papaya (FAO, 2014) and the states of Bahia and Espírito Santo account for more than 60% of the domestic production (IBGE, 2015).

Despite its economic importance for several countries, there are some drawbacks to papaya production such as the high prices of hybrid seeds, generally imported from Taiwan, and the narrow genetic base of the crop, which hampers the development of new hybrids because of the small number of cultivars planted in the main producing regions (Santos et al., 2009).

The low genetic variability makes the crop more vulnerable to economic damages (Oliveira et al., 2010). One solution is to develop new cultivars with characteristics of interest for producers and consumers, which begins with crop genetic improvement works.

Knowing the existing genetic variability makes it possible to develop breeding programs to obtain papaya hybrids with increased productivity and quality of fruits and meet the requirements of domestic and international markets. Studies like this can also provide import information to identify progenitors that in future crosses will enable greater segregation and recombination (Cruz et al., 2012).

Multivariate methods have been used for the quantification of genetic divergence, bringing together treatments into several groups through statistical analysis, such that there is homogeneity within each group and heterogeneity among groups (Bertan et al., 2006).

The hierarchical clustering methods and optimization methods stand out among the multivariate techniques. The hierarchical UPGMA method (Unweighted Pair-Group Method Using an Arithmetic Average) uses arithmetic averages of dissimilarity measures. The Tocher optimization method uses the criterion that the distances within each group are always smaller than those of the intergroup (Cruz et al., 2012).

Because of the importance for crop improvement, studies on the genetic diversity have been carried out in different crops such as guava (Pessanha et al., 2011), common bean (Cabral et al., 2011) and coffee (Martins et al., 2016). A number of genetic divergence studies have also been carried out with different accessions of papaya (*Carica papaya* L.) (Ramos et al., 2011; Quintal et al., 2012; Oliveira et al., 2011; Lucena and Dantas, 2015). Therefore, the objective of this study was to evaluate, by means of variables, the genetic variability among 59 accessions of papaya that have not been previously evaluated in studies of genetic diversity.

MATERIALS AND METHODS

The study was conducted at Santa Terezinha Farm (Caliman Agrícola S/A), 19º 23' 28" S latitude and 40º 04' 20" W longitude, 33 m altitude, average annual temperature of 23.4°C and average rainfall of 1.193 mm year^{-1}, between May 2011 and January 2012. Seventeen morphoagronomic variables were evaluated in 59

accessions of papaya belonging to the Germplasm Active Bank of Calimam Agrícola S.A (Table 1).

The experiment was arranged in a randomized block design with two replicates of five hermaphrodite plants per plot. The cultural practices followed the recommendation for the crop (Martins and Costa, 2003).

The first flower insertion height (FFLH, m) was evaluated at 120 days after planting (DAP). At 240 DAP, the following variables were evaluated: First fruit insertion height (FFRH, m); plant height (PLH, m); stem diameter (STD, m); peduncle length (PL, m); leaf length (LEL, m); maximum leaf width (MLEW, m); chlorophyll content (CHLC) - using a CFL-1030 ClorofiLOG® portable chlorophyllometer, according to the manufacturer's instructions (FALKER, 2008); number of commercial fruits (FRN); fruit mass (FRM, kg); fruit length (FRL, m); fruit equatorial diameter (FRD, m); smallest thickness of fruit pulp (STP, m); greatest thickness of the fruit pulp (GTP, m); soluble solids (SS) - measured in 1/4 ripe fruits by direct reading in bench refractometer (ATTAGO, model N1, Tokyo) and expressed as °Brix; internal firmness of the fruit (FRIF, kg cm^{-2}) measured by a penetrometer (Instruthrem, medol PTR-100) at three points equidistant along the thickness of the pulp of a cross-sectioned fruit, using a 7.9 mm diameter tip and expressed as kg cm^{-2}; and estimated first-year yield per plant (YIELD, kg.plt[-1]) obtained by multiplying fruit mass by fruit number. The variables PL, LEL, MLEW and CHLC were evaluated on three fully developed leaves of each plant per access.

Data were examined by the analysis of variance. The multivariate analysis was performed using the Tocher's method and the hierarchical grouping techniques based on the UPGMA method using the generalized distance of Mahalanobis (D^2) as measure of dissimilarity (Cruz et al., 2012).

The number of groups formed by the UPGMA method was determined by the cut-off point in the dendogram as proposed by Mojena (1977), using the equation Pc = m + kdp, where m = the mean distances of the fusion levels corresponding to the stages; K = 1.25; dp = standard deviation. In order to test the efficiency of the hierarchical grouping method, the cophenetic correlation coefficient (CCC) proposed by Sokal and Rohlf (1962) was estimated. The data were analyzed using the computational resources of the Genes program (Cruz, 2016).

RESULTS AND DISCUSSION

There was significant difference at 1% probability level among the means of the papaya accessions for the 17 morphoagronomic variables (Table 2), showing that variability exists among the accessions, which is important for the study of genetic divergence.

The means obtained for FFLH at 120 DAP and FFRH and PLH at 240 DAP were 0.81, 0.96 and 1.58 m, respectively. Knowing the variability for such variables is of great importance to be explored in new breeding programs such as developing plants with lower PLH, FFRH and FFLH for cultivation in protected environment, besides the advantage of obtaining plants with lower FFRH, which favors a longer harvest (Lim and Hawa, 2007).

STD had an overall mean of 0.09 m. According to Silva et al. (2007), the selection of plants with greater STD can result in more productive plants, due to the high genetic correlation between these variables. Therefore, this descriptor must be used to compose selection indices in breeding programs.

Table 1. Accessions of Solo (S) and Formosa (F) groups papaya (*Carica papaya* L.) used in the study of genetic diversity, Linhares, Brazil, 2012.

Number - Name	Group	Number - Name	Group
1 - Caliman MS	S	31 - JS 12 (206)	F
2 - Sunrise Solo 783	S	32 - Califlora 209	S
3 - Costa Rica	F	33 - Golden Tipo Formosa	F
4 - Taiwan ET	F	34 - Short-peduncle-STZ-03	S
5 - Diva	S	35 - STA HEL III 12 A PLT 07	F
6 - Grampola	S	36 - STA HEL III 11 A PLT 08	F
7 - Sunrise Solo	S	37 - STA HEL III 50 A PLT 09	F
8 - Caliman AM	S	38 - STA HEL III 02 A PLT 01	F
9 - Caliman GB	S	39 - STA HEL III 14 A PLT 05	F
10 - Caliman SG	S	40 - STA HEL III 15 A PLT 04	F
11 - Caliman G	S	41 - STA HEL III 04 A PLT 02	F
12 - Sunrise Solo 72/12	S	42 - STA HEL III 12 A PLT 06	F
13 - Kapoho Solo Polpa Amarela	S	43 - Papaya 42 Formosa	F
14 - Baixinho de Santa Amália	S	44 - Papaya 45 Formosa Roxo	F
15 - Sunrise Solo TJ	S	45 - Papaya 46 Claro	F
16 - Tailandia	F	46 - Caliman Fruto Médio Verde	S
17 - São Mateus	S	47 - Golden Robusto	S
18 - Kapoho Solo Polpa Vermelha	S	48 - JS 11 (210)	F
19 - Sunrise solo (Progeny Tainung)	S	49 - Tainung 01 F_1	F
20 - Waimanalo	S	50 - STZ 23 Pedúnculo Longo	S
21 - Mamão Bené	F	51 - STZ 63	F
22 - Mamão Roxo	S	52 - Sekati Macuco	F
23 - Maradol (Source Mexico)	F	53 - Gran Golden	S
24 - Maradol (Grande Limão)	F	54 - Sunrise Solo Paulo Brunelle	S
25 - Sekati	F	55 - THB STZ-39	S
26 - Baixinho Super	S	56 - Incaper 39	F
27 - Americano	F	57 - B5 Geraldo	F
28 - STZ 51	S	58 - Formosa Golden	F
29 - 206/4	F	59 - Formosa Brilhoso	F
30 – Calimosa F_1	F		

CHLC had an overall mean of 52.65. Castro et al. (2014) investigated papaya genotypes with different leaf colors and found that the chlorophyll indexes (CHI) quantified are related to the total concentration of chlorophyll quantified by the destructive method. This result suggests that the higher the chlorophyll content, the greater the photosynthetic capacity and, consequently, the greater the increase in yield.

FRM had overall mean of 0.93 kg, ranging from 0.21 to 2.31 kg per fruit, for the accessions short-peduncle-STZ-03 of the Solo group and Maradol (Grande Limão) of the Formosa group, respectively. These results were close to those found by Quintal et al. (2012), who reported overall mean of 0.7017 kg for papaya genotypes also of the groups Solo and Formosa. Fruit mass is a useful variable for selection of plants that express good yield and is used in the separation of the heterotic groups Solo and Formosa.

The varieties of the Solo group are planted in many regions of the world, producing fruit with desirable characteristics for export, with red flesh, small size and weight between 300 and 650 g. Fruits of the Formosa group have red flesh and average size between 1000 and 1300 g. According to Oliveira et al. (2011), the Formosa group consists of commercial hybrids that have gained space in domestic and foreign markets, with strong sales growth in Europe, Canada and the United States.

Regarding fruit size, the variable FRD had mean of 0.10 m, varying from 0.07 m (Sunrise Solo 783) up to 0.15 m (Formosa Brilhoso) and the variable FRL had mean of 0.19 m, ranging from 0.11 m (short-peduncle-STZ-03) to 0.39 m (Americano), with the minimum values represented by the accession Solo group and maximum by the Formosa group, respectively. The fruit size in papaya has also been used to differentiate the heterotrophic groups Solo from Formosa. These

Table 2. Summary of the analysis of variance of the morphological variables of plants and the physical and chemical variables of fruits with the respective mean square of the treatment (MStrat), mean square of the residue (MSres), means, maximum (Max.), minimum (Min.), coefficient of experimental variation (CVe), estimate of coefficient of genetic variation (CVg), and coefficient of genotypic determination (H²) for the 59 accessions of *Carica papaya* L.

Variable	MStrat	MSres	Means	Max.[1]	Min.[1]	CVe (%)	CVg (%)	H²
FFLH	375.64**	24.33	0.81	1.10 (49)	0.52 (14)	6.07	16.31	87.83
FFRH	583.02**	74.21	0.96	1.31 (49)	0.58 (26)	8.84	16.56	77.41
PLH	1233.45**	161.2	1.58	2.07 (7)	0.98 (14)	8.04	14.67	76.88
STD	2.84**	0.84	0.09	0.14 (17)	0.07 (9)	10.31	11.2	54.09
PL	139.97**	20.68	0.72	0.89 (32)	0.37 (34)	6.33	10.74	74.25
LEL	61.23**	13.53	0.41	0.62 (32)	0.26 (34)	9.03	11.99	63.79
MLEW	104.71**	31.92	0.57	0.73 (41)	0.38 (34)	9.83	10.5	53.27
CHLC	26.29**	3.35	52.65	59.48 (22)	42.37 (8)	3.47	6.43	77.36
FRN	128.31**	21.2	15.58	41.75 (34)	2.50 (48)	29.55	46.96	71.63
FRM	585330.09**	32330.5	0.93	2.31 (24)	0.21 (34)	19.26	56.32	89.53
FRL	66.36**	11.39	0.19	0.39 (27)	0.11 (34)	17.76	27.59	89.53
FRD	6.09**	0.43	0.10	0.15 (59)	0.07 (2)	6.69	17.08	86.67
STP	56.25**	6.59	0.02	0.033 (37)	0.012 (58)	13.16	25.52	78.00
GTP	68.10**	5.72	0.03	0.039 (23)	0.018 (30)	8.76	20.46	84.48
FRIF	1.67**	0.45	10.09	12.27 (41)	8.69 (35)	6.67	7.73	57.30
SS	2.71**	0.74	9.66	12.06 (45)	7.39 (23)	8.91	10.26	56.99
YIELD	49.32**	18.44	11.46	28.57 (36)	3.14 (41)	37.46	34.26	45.55

** Significant at 1% probability by the test F. [1] Numbers in parentheses correspond to accession identification: 2, 'Sunrise Solo 783'; 7, 'Sunrise Solo'; 8, 'Caliman AM'; 9, 'Caliman GB'; 14, 'Baixinho de Santa Amália'; 17, 'São Mateus'; 23, 'Maradol (Source Mexico)'; 24, 'Maradol (Grande Limão)'; 26, 'Baixinho Super'; 27, 'Americano'; 30, 'Calimosa' F_1; 32, 'Califlora 209'; 34, 'short-peduncle-STZ-03'; 35, 'Santa Helena III Trat 12A PLT.07'; 36, 'Santa Helena III Trat 11A PLT.08'; 37, 'Santa Helena III Trat 50A PLT.09'; 41, 'Santa Helena III Trat 04A PLT.02'; 45, 'Papaya 46 Claro; 48, 'JS 11(210)'; 49, 'Tainung 01' F_1; 58, 'Formosa Golden'; 59, 'Formosa Brilhoso'.

variables are important in the process of transport and packaging of fruit.

The mean for FRIF was 10.09 kg cm^{-2}. This is important information, since this variable is considered an attribute of quality indicating the maturation stage of fruit or harvesting point, which has direct influence on commercialization. Morais et al. (2007) argue that fruit firmness establishes the post-harvest life, since low firmness results in fruit less resistant to transportation, storage and handling.

SS content had overall mean of 9.66°Brix. These results corroborate with those found by Ocampo et al. (2006) and Oliveira et al. (2010) in studies of papaya germplasm and those reported by Marin et al. (2006) in hybrid analysis. SS content may indicate the fruit harvesting point, since there is a relation between them and the maturation stage of the fruit. It is known that during the maturation phase, fruits increase the sugar content, which varies with the type of papaya, cultivar, climatic conditions, soil fertility, production time, and stage of development and maturation (Fontes et al., 2012).

The coefficients of experimental variation (CVe) ranged between 3.47 and 37.46% for the variables CHLC and YIELD, respectively. It was found that 87% of the variables had CVe below 20%, indicating a good experimental precision (Ferreira et al., 2016). These results corroborate with those found by Dias et al. (2011), who analyzed papaya descriptors and found coefficients of experimental variation ranging from 3.09 to 50.29% and that 80% of the variables evaluated had coefficients below 20%.

The genetic variation coefficients (CVg) were high for FRM (56.32%), FRN (46.96%), YIELD (34.26%) and FRL (27.59%) indicating that the variation occurring among the accessions are due to their genetic constitution. This genetic parameter is an important indicator of the relative magnitude of the possible changes that can be obtained in each variable through selection and has been used for peduncle length and number of fruits per plant (Oliveira et al., 2010), plant height and number fruits (Silva et al., 2008) in papaya.

The genotypic determination coefficients (H^2) were higher than 80% for the variables FFLH, FRM, FRL, FRD, and GTP. These results indicate that breeding programs can achieve genetic progress and increase the papaya yield through a simple selection process.

The variables YIELD, SS, MLEW and STD had lower H^2 values showing the influence of the environment on the expression of these variables. An alternative in such cases is the use of indirect selection, through genetic and/or phenotypic correlation.

Table 3. Clustering of the 59 accessions of *Carica papaya* L. by the Tocher method, using the generalized distance of Mahalanobis as measure of genetic distance.

Groups	Acessions[1]
I	12; 15; 19; 7; 1; 5; 4; 28; 50; 11; 10; 58; 51; 6; 57; 18; 45; 8; 9; 54; 47; 33; 2; 13; 55; 3; 30; 22; 43; 49; 17; 21; 29; 20; 35; 31; 59
II	14; 26; 44; 36; 56; 23; 25; 52; 48; 40; 16; 24; 38; 41; 42; 39; 37
III	27
IV	32
V	34

Acessions[1]: 1 - 'Caliman MS'; 2, 'Sunrise Solo 783'; 3, 'Costa Rica'; 4, 'Taiwan ET'; 5, 'Diva'; 6, 'Grampola'; 7, 'Sunrise Solo'; 8, 'Caliman AM'; 9, 'Caliman GB'; 10, 'Caliman SG'; 11, 'Caliman G'; 12, 'Sunrise Solo(72/12)'; 13, 'Kapoho Solo polpa amarela'; 14, 'Baixinho de Santa Amália'; 15, 'Surise Solo TJ'; 16, 'Tailândia'; 17 - 'São Mateus'; 18, 'Kapoho Solo polpa vermelha'; 19, 'Sunrise Solo (Progeny Tainung)'; 20, 'Waimalano'; 21, 'Mamão Bené'; 22, 'Mamão Roxo'; 23, 'Maradol (Source Mexico)'; 24, 'Maradol (Grande Limão)'; 25, 'Sekati'; 26, 'Baixinho Super'; 27,'Americano'; 28, 'STZ-51'; 29 - '206/4'; 30, 'Calimosa' F_1; 31, 'JS 12 (206)'; 32, 'Califlora 209'; 33, 'Golden Tipo Formosa'; 34, 'short-peduncle-STZ-03'; 35, 'Santa Helena III Trat 12A PLT.07'; 36, 'Santa Helena III Trat 11A PLT.08'; 37, 'Santa Helena III Trat 50A PLT.09'; 38, 'Santa Helena III Trat 02A PLT.01'; 39, 'Santa Helena III Trat 14A PLT.05'; 40, 'Santa Helena III Trat 15A PLT.04'; 41, 'Santa Helena III Trat 04A PLT.02'; 42, 'Santa Helena III Trat 12A PLT.06'; 43, 'Papaya 42 Formosa'; 44, 'Papaya 45 Formosa Roxo'; 45 - 'Papaya 46 Claro'; 46, 'Caliman Fruto Médio Verde'; 47, 'Golden Robusto'; 48, 'JS 11(210)'; 49, 'Tainung 01' F_1; 50, 'STZ 23 Pedúnculo Longo'; 51 - 'STZ 63'; 52, 'Sekati Macuco'; 53, 'Gran Golden'; 54, 'Sunrise Solo Paulo Brunele'; 55, 'THB STZ 39'; 56, 'Incaper 39'; 57, 'B5 Geraldo'; 58, 'Formosa Golden'; 59, 'Formosa Brilhoso'.

The Tocher optimization clustering method using Mahalanobis distances separated the accessions into five groups, with similar behavior within the group and divergent among groups (Table 3). This is an optimization technique that groups individuals by maintaining the criterion that intra-group distances are always smaller than inter-group distances (Cruz et al., 2012).

Group I was formed by 62.71% of the accessions, with large part belonging to the Solo group and accessions of the Formosa group such as Tainung 01, Calimosa, Golden Tipo Formosa, and Formosa Brilhoso. This indicates that although they were of different heterotic group, the set of variables through the multivariate analyzes clustered them in the same group.

Group II consisted of 27% of accessions, including accessions from the groups Solo and Formosa (Baixinho de Santa Amália, Baixo Super, Papaya 45 Formosa Roxo, Santa Helena III Trat 11A PLT.08, Incaper 39, Maradol (Grande Limão), Sekati, Sekati Fruto Longo Macuco, JS 11 (210), Santa Helena III Trat 15A PLT.04, 16 - Tailandia, 24 - Maradol (Grande Limão), St. Helena III Trat 02A PLT.01, Santa Helena III Trat 04A PLT.02, Santa Helena III Trat 12A PLT.06, Santa Helena III Trat 14A PLT.05, Santa Helena III Trat 50A PLT.09). These results are similar to those found by Barbosa et al. (2011), who investigated the divergence among papaya accessions using artificial intelligence resources and found no separation of the accessions of the groups Solo and Formosa in the groups formed by the Tocher method.

Groups III, IV and V are formed by the single accessions Americano, Califlora 209 and short-peduncle-STZ 03 respectively, showing that these are the most divergent genotypes. This occurred because of a certain variable or set of variables that allowed the formation of isolated groups; supposedly, the variable of maximum value for FRM of the accession Americano, maximum value for PL and LEL for Califlora and the minimum values for PL, LEL, FRL, and FRM, and maximum for FRN of accession short-peduncle-STZ 03.

These results are promising for future crosses, since accessions clustered in different groups are more divergent and are an essential source for obtaining hybrids. According to Santos et al. (2012), crosses from genotypes grouped in divergent groups are considered more promising by possibly being more dissimilar and consequently providing greater heterotic effect on the following generations.

The Singh's method was used to demonstrate the relative importance of the 17 morphoagronomic variables for genetic diversity among the papaya accessions (Table 4). The variables FRM (16.88%), FRD (11.32%) and GTP (11.01%) showed the greatest contribution to genetic diversity. On the other hand, YIELD (2.26%), STD (1.17%) and FFRH (0.66%) showed the smallest relative contribution. These results corroborate with those found by Lucena and Dantas (2015), indicating that the variables with less importance express less variability.

Figure 1 shows the dissimilarity among the accessions by the UPGMA method. This method has the advantage of not working with extreme values, minimum and maximum values, but is based on the arithmetic average of the data.

The cut at the distance of 46.35% based on the Mojena's (1977) criterion allowed the formation of six groups of dissimilarity. Group I was formed by 67% of the total number of accessions evaluated, similar to that obtained by the Tocher's method (Table 3). This group is formed by a large part of the accessions of the Solo group.

The accessions 14 - Baixinho de Santa Amália, 26 – Baixo Super, 36 - STA HEL III 11A, and 44 – Papaya 45

Table 4. Relative contribution of 17 morphoagronomic variables to diversity, using the Singh's (1981) criterion based on D^2 of Mahalanobis.

Variable	S.j	Value in %
FFLH	41939.33	10.02
FFRH	2771.55	0.66
PLH	25808.41	6.17
STD	4934.47	1.17
PL	21913.04	5.23
LEL	10769.71	2.57
MLEW	25749.87	6.15
CHLC	26668.25	6.37
FRN	15111.40	3.61
FRM	70609.70	16.88
FRL	20588.29	4.92
FRD	47366.23	11.32
STP	14030.88	3.35
GTP	46055.21	11.01
FRIF	20395.91	4.87
SS	14077.19	3.36
YIELD	9475.13	2.26

Formosa Roxo form the Group II, which includes the accessions with the minimum value for the variables FFLH (0.52 m), FFRH (0.58 m) and PLH (0.97 m). Among these accessions, Baixinho de Santa Amália has short height and is early flowering; which are favorable variables for hybridization works aiming to improve the precocity of current cultivars (Lim and Hawa, 2007).

The Group III is formed by a single accession of the Formosa group (32 - Califlora 209), therefore one of the most divergent accessions, showing maximum values for PL (0.89 m) and LEL (0.62 m).

Group IV includes the accessions 25 - Sekati, 52 - Sekati Fruto Longo Macuco, 23 - Maradol (Origin Mexico), 56 - Incaper 39, 24 - Maradol (Grande Limão), 40 - STA HEL III 15 A, 37 - STA HEL III 50 A, 39 - STA HEL II 14 A, 41 - STA HEL III 4A, 42 - STA HEL III 12 A-06, 38 - STA HEL III 02A and 16 - Tailandia. It is likely that the combination of a set of variables as well as the same genetic base allowed to cluster in a single group the accessions of the Formosa group.

Groups V and VI were formed by the single accessions 27 - Americano and 34 – short-peduncle-STZ 03, respectively, indicating that these accessions as well as 32 - Califlora 209 of Group III are the most divergent in the germplasm bank and can be used as parents in future breeding work to obtain new hybrids.

In this study, the grouping of the accessions by the UPGMA method was similar to the group formation by the Tocher's optimization method. The similarity between these two techniques can be verified by the fact that accessions 32 - Califlora 209, 27 - Americano and 34 - short-peduncle-STZ-03 form single-accession groups using both clustering methods (Table 3 and Figure 1).

Silva et al. (2014) concluded the agreement between multivariate and clustering techniques is important in the study of genetic diversity, since it makes possible the recommendation of crosses between more divergent parents, aiming to broaden the genetic base and, consequently, increase variability. However, this recommendation should also take into account the behavior of each genotype, having greater importance those that show superior performance for the morphoagronomic variables of interest.

Based on the results of this study, it is expected that from the crossing between one of the three more divergent accessions with any other accession belonging to the other groups, which presents variables of agronomic importance, may contribute to improvement works and, therefore, increase papaya yield.

Conclusions

The variables plant height, first fruit insertion height, greatest thickness of fruit pulp, fruit diameter, and fruit length had high heritability indicating expressive gains in the simple process of selection.

There is genetic variability among the accessions of *Carica papaya* L., and the accessions Americano, short-peduncle-STZ-03 and Califlora 209 are the most divergent ones. The Tocher's optimization and hierarchical UPGMA methods were partially concordant in the formation of groups of the papaya accessions. The variables fruit mass, fruit diameter and plant height were
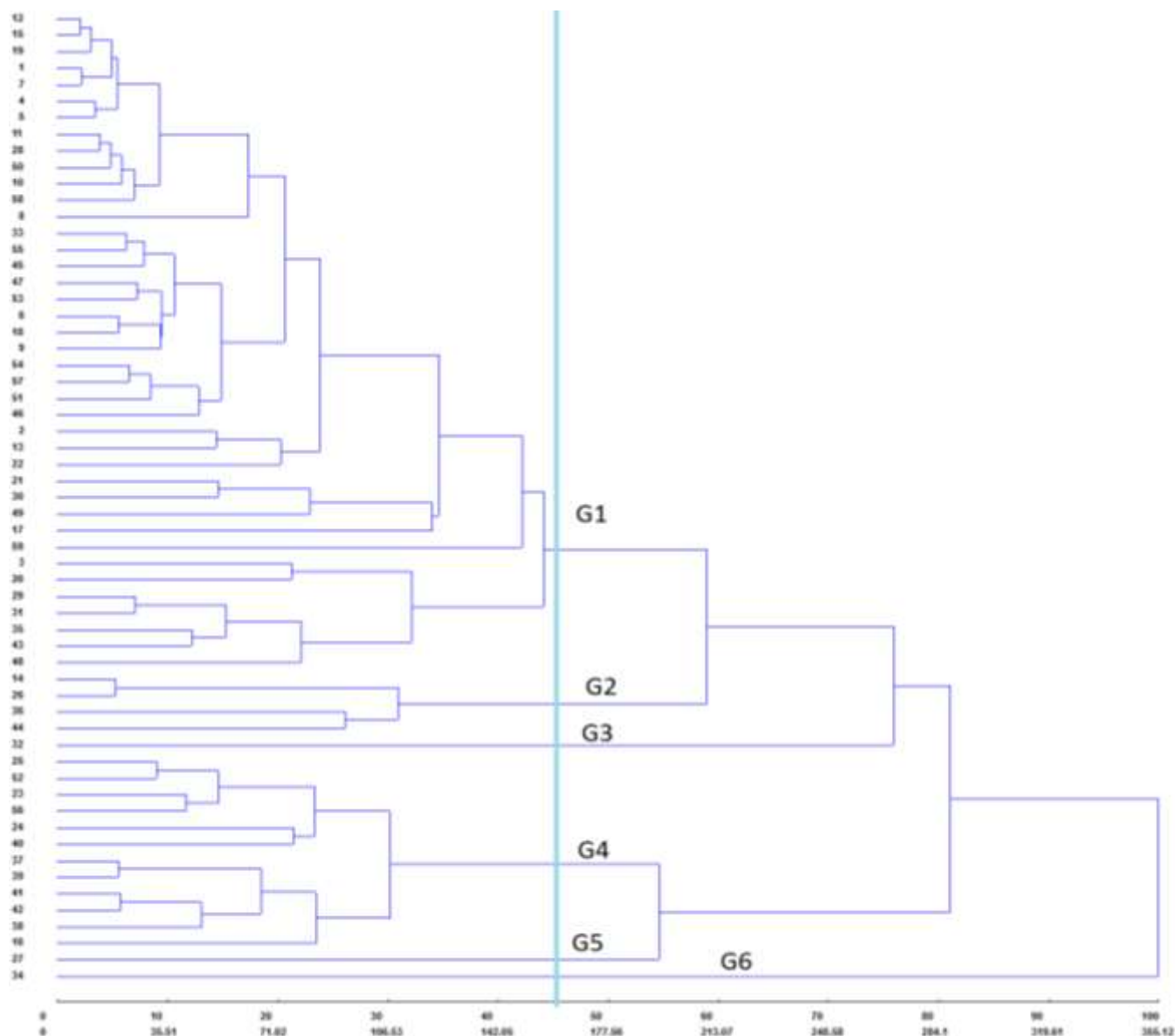
Figure 1. Dendrogram of the analysis of 59 accessions of papaya obtained with the UPGMA method and the Mahalanobis distance as a measure of genetic dissimilarity. The cophenetic correlation coefficient (r) is 0.74** (Acessions: 1 - 'Caliman MS'; 2, 'Sunrise Solo 783'; 3, 'Costa Rica'; 4, 'Taiwan ET'; 5, 'Diva'; 6, 'Grampola'; 7, 'Sunrise Solo'; 8, 'Caliman AM'; 9, 'Caliman GB'; 10, 'Caliman SG'; 11 - 'Caliman G'; 12, 'Sunrise Solo(72/12)'; 13, 'Kapoho Solo polpa amarela'; 14, 'Baixinho de Santa Amália'; 15, 'Surise Solo TJ'; 16, 'Tailândia'; 17 - 'São Mateus'; 18, 'Kapoho Solo polpa vermelha'; 19, 'Sunrise Solo (Progeny Tainung)'; 20, 'Waimalano'; 21, 'Mamão Bené'; 22, 'Mamão Roxo'; 23, 'Maradol (Source Mexico)'; 24, 'Maradol (Grande Limão)'; 25, 'Sekati'; 26, 'Baixinho Super'; 27,'Americano'; 28, 'STZ-51'; 29 - '206/4'; 30, 'Calimosa' F$_1$; 31, 'JS 12 (206)'; 32, 'Califlora 209'; 33, 'Golden Tipo Formosa'; 34, 'short-peduncle-STZ-03'; 35, 'Santa Helena III Trat 12A PLT.07'; 36, 'Santa Helena III Trat 11A PLT.08'; 37, 'Santa Helena III Trat 50A PLT.09'; 38, 'Santa Helena III Trat 02A PLT.01'; 39, 'Santa Helena III Trat 14A PLT.05'; 40, 'Santa Helena III Trat 15A PLT.04'; 41, 'Santa Helena III Trat 04A PLT.02'; 42, 'Santa Helena III Trat 12A PLT.06'; 43, 'Papaya 42 Formosa'; 44, 'Papaya 45 Formosa Roxo'; 45, 'Papaya 46 Claro'; 46, 'Caliman Fruto Médio Verde'; 47, 'Golden Robusto'; 48, 'JS 11(210)'; 49, 'Tainung 01' F$_1$; 50, 'STZ 23 Pedúnculo Longo'; 51 - 'STZ 63'; 52, 'Sekati Macuco'; 53, 'Gran Golden'; 54, 'Sunrise Solo Paulo Brunele'; 55, 'THB STZ 39'; 56, 'Incaper 39'; 57, 'B5 Geraldo'; 58, 'Formosa Golden'; 59, 'Formosa Brilhoso').

the major contributors to genetic diversity.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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